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June 3, 2003, 15:00:18 ; Search time 22 Seconds (without alignments) 450.584 Million cell updates/sec
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1274
1 MVSKGEELFTGVVPILVELD......VLLGFVTAAGITLGMDELYK 239
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GenCore version 5.1.6 Copyright (c) 1993 2003 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                     112892 seqs, 41476328 residues
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Mäximum Match 100%
Listing first 45 summaries
                                                                          OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Perfect score:
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		d			SUMMARIES	
Result		Query				
NO.	Score	Match	Match Length	80	ea	Description
П	1247	97.9	238	П	GFP_AEQVI	P42212 aequorea vi
7	91.5	7.2	861	-	SYL_HAEIN	P43827 haemophilus
m	89.2	7.0	879	,-4	SYL_XYLFA	Q9pbg8 xylella fas
4	87.5	6.9	2222	-	DPOE_YEAST	P21951 saccharomyc
S	87	6.8	874	-	SLAP_BACLI	P49052 bacillus li
9	86.5	6.8	533	r-4	CP51_CANGA	P50859 candida gla
7	86.5	6.8	795	-	D152_HAEIN	haemoph
œ	86.5	9.9	797	-	D151_HAEIN	P46024 haemophilus
6	8	6.8	357	-1	TRMA_CAMJE	O9pp92 campylobact
10	85.5	6.7	788	-	DPOL_HPBHE	
11	85.5	6.7	793	-	D153_HAEIN	
12	•	6.7	988	~	ITH3_MESAU	. –
13		6.7	941	7	GUN_BACS6	P19424 bacillus sp
14	82	6.7	439	-	SY62_DISOM	P24506 discopyge o
15	84.5	•	613		PEPF_MYCPU	
16	84	9.9	353	~	HIS7_BUCAI	
17	m.	9.9	504		YC03_KLEPN	048449 klebsiella
18	83.5	9.9	538	-	GRBE_RAT	O88900 rattus norv
19	83.5	9.9	658	7	ADAS_HUMAN	000116 homo sapien
20	83.5	9.9	1164	~	BAG_STRAG	P27951 streptococc
21	83	6.5	461	7	PSBC_CYAPA	-
22	83	6.5	774	-	AMY 2_SCHPO	042918 schizosacch
23	82.5	6.5	533	~	NIFD_CLOPA	P00467 clostridium
24	82	6.4	682	-	PRC_ECOLI	P23865 escherichia
25	82	6.4	752	~1	NEC1_RAT	P28840 rattus norv
56	81	6.4	336	-	YD48_METJA	Q58743 methanococc
27	. 81		1224	-	COPA_HUMAN	Η.
28	80.5	•	393	-	MT04_HELPY	
29	80.5	٠	658	,-,	ADAS_CAVPO	P97275 cavia porce
30	80,5	٠	860	_	SYL_ECOLI	
31	80	6.3	461	,-,	PSBC_CHLEU	-
32	80	6.3	737	-	OPT1_DROME	_
33	79.5	6.2	312	-	TRXB_CHIMU	Q9pkt7 chlamydia m

P94126 azorhizobiu P36924 bacillus ce P17655 homo sapien Q63416 rattus norv Q97146 clostridium P03162 duck hepatil P53917 saccharomyc P07354 gallus gallus P39321 escherichia P39321 escherichia P39358 escherichia	ENTS	238 AA. update) n'update)	pa; Hydroida; Leptomedusae;	VENCE. W.W., Prendergast F.G., victoria green-fluorescent	; ein. Expression of the gene and the recombinant protein.";	, Prendergast F.G., Ward W.W.; le chromophore of the Aequorea	MS). Gross L.A., Tsien R.Y., victoria green fluorescent	Jr.; ifluorescent protein."; if). OMS) OF MUTANT WITH YELLOW ENMISSION. io K., Hanson G.T., Remington S.J.; ifts in the yellow-emission variants
AZOCA BACCE HUMAN ROLONB CLONB HPBDU YEAST CHICK ECOLI ECOLI	alignments	T; nce u ation	Hydrozoa;	SEQ rd rd	; ein. the 1	, W.M. eptic	0 0	SSTROMS; 187. Jr. 1996). (1996). SSTROMS; 351; Xallio Ashifts
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непенененен		eeat st n.	yfis) darid	D PARTIMED P	d-81; cent stic:	d=84, Westhe In.	1.9 ANG-8703 Kallio he Aeq	1.9 111pp 111pp 6-12 6-12 8-97 8-97 8-97 998)
468 546 700 887 431 431 835 953 1259 1148 1148		NDAR 32, 32, 40, Prot	(Jell) () Cnl	N.A., AND 227; PubMed Eckenrode ture of the control	F.L., PubMed-8137953; F.L., Fluorescent protein. Tacteristics of the 77-280(1994).	PubMe D.C. e of prote	5	Pubmed-9631087; Pubmed-9631087; Phillips G.N. Jr. ucture of green flu. 4:1246-1251(1996). Pubmed-9782051; Liger M.A., Kallio K of spectral shifts nt protein.; 1771989.
		STA .04; (Rel. (Rel. (Rel.	toria fetazoa Aeguo	M N.A. 15527; , Ecke ; ucture	ROM N.A. 185810; Tsuji F Freen fl	ME. 3192221; Pu Prasher I structure prescent pr	CRYSTALLOGRAPHY (1.9- IB-9655565; Pubmed-87 M. Cubitt A.B., Kall Iton S.J.; al structure of the A. in structure of the A. in structure of the A.	ALLOGRA is L.G. ar str mol. 1 mol. 1 5509; 5509; basis 1267-1
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Query Match
Best Local Similarity 98.33
Matches 234; Conservative
                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                        NCBI_TaxID=727;
                                                                                                                                                                                         Leucyl-tRNA sy
LEUS OR HI0921
                                                                                                                                                                                                                                                                                                                Venter J.C.;
                                                                                                                                                       SYL_HAEIN
P43827;
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                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its was by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                               MEDLINE-99238303; Pubmed-10220315;
Elsliger M.A., Wachter R.M., Hanson G.T., Kallio K., Remington S.J.;
"Structural and spectral response of green fluorescent protein
                                                                                                                                                                                                     WWW="http://www.expasy.org/spotlight/articles/sptlt011.html".
                                                                                                                                                                                                                                                                                                                                                                                                                              MODIFIED TO FORM THE CHROMOPHORE.
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L -> M.

L -> M.

V -> I.

N -> Q (IN REF. 2).

D -> P (IN REF. 2).

E -> P (IN REF. 2).

E -> P (IN REF. 2).
       X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
                                                                                                                                                                                                                                                                                                                                                                                              Green_fl_protein.
                                                                                                                                                                                                                                                                                                                                                                                                          PR01229; GFLUORESCENT.
PD013756; Green_fl_protein; 1.
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219
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172
238 AA;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EBML outstation the European Bioinformatics in Stitute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                               62 VTTLSYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLV 121
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                                                                                                                                           61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Whole-genome random sequencing and assembly of Haemophilus influenzae
                                                                                                                                                                                   2 VSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPTL
                                                                            Gaps
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STRAINER KNY20 / ATCC 51907;

MEDLINE-95536630; PubMed-7542600;

Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,

Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,

McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,

Scott J.D., Shirley R., Lu L. I., Glodek A., Kelley J.M.,

Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,

Otterback T.R., Hanna M.C., Nguyen D.T., Sandek D.M., Brandon R.C.,

Fine L.D., Fritchman J.L., Eubmann J.L., Geoghagen N.S.M.,

Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
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-!- CATALYTIC ACTIVITY: ATP + L-leucine + tRNA(Leu) - AMP + diphosphate + L-leucyl-tRNA(leu).
-! GADDANTE + L-leucyl-tRNA(leu).
-! SUBUNIT: MONOMER (BY SIMILARITY).
-!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- SIMILARITY: BELONGS TO CLASS-I AMINOACYL-TRNA SYNTHETASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
15-UTN-2002 (Rel. 41, Last annotation update)
Leucyl-tRNA synthetase (EC 6.1.1.4) (Leucine--tRNA ligase) (LeurS).
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Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
Length 238;
                                                                     Indels
       DB 1;
       Score 1247; DB 1;
Pred. No. 1.1e-99;
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                                                                     1; Mismatches
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TIGRFAMS; TIGR00396; leus_bact; 1.
PROSITE; PS00178; AA_TRNA_LIGASE_I; 1.
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IPR002300; tRNA-synt_la,
IPR001412; tRNA-synt_I.
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   97.9%;
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11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            409 GKRQVNYRLRDWGVSRQRYWGAPIPMLTLENGDVVPA-----PMEDLPIILPEDVVMD 461
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Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
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16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Leucyl-tRNA synthetase (EC 6.1.1.4) (Leucine--tRNA ligase) (LeuRS).
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"The genome sequence of the plant pathogen Xylella fastidiosa.";
Nature 406:151-159(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group;
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                                                                                                                                                                                                                                                        7.2%; Score 91.5; DB 1; Length 861; 24.1%; Pred. No. 3.6;
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ATP (BY SIMILARITY).
EB93304F6B4C8FB7 CRC64;
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                                                                          "HIGH" REGION.
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MEDLINE-20365717; PubMed-10910347;
                                                                          52 "F
623 "R
622 AT
97750 MW;
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Xylella fastidiosa.
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                                           Complete proteome
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09PBG8;
                                                                                                                                                     BINDING
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                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                              Matches
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              50 TTGKLPVPWPTLVTTLSYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNY-- 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 154 MADKQKNG-IKVNFKIRHNIEDGSVQLADHYQQNTPI------GDGPVLLPDN 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ------KTRAEVKFEGDTLVNRIELKGIDFKEDGNILGHKLEYNYNSHNVYI 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  321 TNEQLEV-WVANFVLMAYGTGAVMAVPGHDQRDQEF--ANKYGLFIRQVIALKEPKNQDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   378 STWEPDVWRDWYADKTR---EFE---LINSAEFDGLDYQDAFEVLAERFE-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00133; tRNA-synt_1; 1.
PRINTS; PR00985; TRNASYNTHLED.
TIGREMAS; TIGRO0396; LOUS_bact.1.
PROSTIE; PS001789; AA_TRNA_LIGASE_1; 1.
Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                    diphosphate + L-leucyl-tRNA(Leu).
SUBCELLULAR LOCATION: Cytoplasmic.
SIMILARITY: BELONGS TO CLASS-1 AMINOACYL-TRNA SYNTHETASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                57;
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16-CCT-2001 (Rel. 40, Last annotation update)
16-CT-201 (Rel. 40, Last annotation update)
18-CT-201 (Rel. 40, Last annotation update)
19-CT-201 (Rel. 40, Last annotation update)
18-CT-77 (DNA POLY OR PULZ OR VILZ62W OR NO825.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 7.0%; Score 89.5; DB 1; Length 879; Best Local Similarity 22.2%; Pred. No. 5.4; Matches 44; Conservative 29; Mismatches 68. Thanh
CATALYTIC ACTIVITY: ATP + L-leucine + tRNA(Leu) - AMP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "KMSKS" REGION.
ATP (BY SIMILARITY).
9FDCCB992092919E CRC64;
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MEDLINE-90381771; PubMed-2169349;
MORTISON A., Araki H., Clark A.B., Hamatake R.K., Sug
Mortison A., Araki H., Clark A.B., Hamatake R.K., Sug
Mortison A., Araki D. Olymerase in S. Cerevisiae.";
Cell 62:1143-1151(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Saccharomycetales; Saccharomycetaceae; Saccharomyces
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InterPro; IPR002302; Leu-trhAsyptla.
InterPro; IPR002300; TRNA-synt.la.
InterPro; IPR001412; tRNA-synt.la.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-S288c / FY1679;
MEDLINE-96310631; PubMed-8740425;
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P21951;
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STANDARD;
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874 AA;
                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                               01-FEB-1996
01-NOV-1997
                       SLAP_BACLI
P49052;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
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                               UAREPERSONSESTATETERS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its was by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseelisb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             54 LPVPWP-TLVTTLSYGVQCFSRYPDHM------KQHDFFKSAMPEGYV----OERTI 99
                                                                                                                                                                                                                                                                                                                                                                                                       -!- CATALYTIC ACTIVITY: N deoxynucleoside triphosphate - N diphosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                883 LPRSFPETYFFTLENGKKLYLSYPCSMLNYRVHQKFTNHQYQELKDPLNYIYETHSENTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBGULT: CONSISTS OF FIVE SUBUNITS (200 kDa, 80 kDa, 34 kDa, 30 kDa, AND 29 kDa).
SUBCELLULAR LOCATION: Nuclear.
DOMAIN POLYMERASE ACTIVITY DOMAIN RESIDES IN THE
N-TERMINAL HALF OF THE PROPERN, WHILE THE C-TERMINUS IS NECESSARY
FOR COMPLEXING SUBUNITS B AND C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MISCELLANEOUS: IN EUKARYOTES THERE ARE FIVE DNA POLYMERASES:
ALPHA, BETA, GAMAA, DELTA, AND EPSILON WHICH ARE RESPONSIBLE FOR
SIMILARITY: BELONGS OF DNA SYNTHESIS.
SIMILARITY: BELONGS TO AN POLYMERASE TYPE-B FAMILY. HIGH
SIMILARITY MITH MAMMALIAN DNA POLYMERASE EPSILON.
Sen-Gupta M., Lyck R., Fleig U., Niedenthal R.K., Hegemann J.H.; *The sequence of a 24,152 bp segment from the left arm of chromosome XIV from Saccharomyces cerevisiae between the BNI1 and the POL2
                                                                                                                                                                                                                                                    *DNA polymerase II, the probable homolog of mammalian DNA polymerase epsilon, replicates chromosomal DNA in the yeast Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14; Mismatches 49; Indels 31; Gaps
                                                                                                                                                                                                                                                                                                                                                       1- FUNCTION: DNA POLYMERASE II PARTICIPATES IN CHROMOSOMAL DNA
                                                                                                                                                                                                       Araki H., Ropp P.A., Johnson A.L., Johnston L.H., Morrison A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 6.9%; Score 87.5; DB 1; Length 2222; Best Local Similarity 28.2%; Pred. No. 25; Matches 37; Conservative 14; Mismatches 49; Indels 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     644 644 M -> I (IN POL2-9 TS MUTANT).
710 710 P -> S (IN POL2-18 TS MUTANT).
2222 AA; 255669 MW; CBCDDE2AB147D65B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS00116; DNA_POINMERASE_B; FALSE_NEG.
Iransferase; DNA-directed DNA polymerase; DNA replication;
DNA-binding; Zinc-finger; Nuclear protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL.
                                                                                                                                                     TEMPERATURE SENSITIVE MUTANTS.
MEDLINE~92164663; PubMed~1537345;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SGD; SG005206; POL2.
InterPro; IPRO02064; DNA_pol_B.
Pfam: PF00136; DNA_pol_B; 1.
PRINTS; PRO0106; DNAPOLB.
SMART; SMO0486; POLBC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; M60416; AAA88711.1; -. EMBL; X92494; CAA63235.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; 271538; CAA96169.1; -. PIR; A36028; A36028.
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                                                                                                                                                                                                                                                                                                                               J. 11:733-740(1992).
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                                                                                                  east 12:505-514(1996).
                                                                                                                                                                                                                                                                                                                                                                                    REPLICATION
                                                                                                                                                                                                                                                                                                                                                                                                                                       (DNA) (N)
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                                                                                                                                                                                                                                                                                                       cerevisiae
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZN_FING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VARIANT
                                                                                                                                                                                                                                  Sugino
                                                                               Paner
                                                                                                                                                                                                                                                                                                                                  EMBO
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     NAMES OF THE STANDARD OF THE S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              611 KSNIGHEAPRLELVSKAGQKGEAADTTLGAGNTVAYQLSNYTTEGVYADAADLAGY--FF 668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98 TIFFKDDGNYKTRAEVKFEGDTLVNRIELKGID---FKEDGNILGHKLEYNYNSHNVYIM 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             155 ADKQK----IEDGSVQLADH 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            722 SVKFKDVEVEQFENRKVNIDRVLDVVKSDKDDVLNGIKLNISTEHKVRIVDEGTEG---- 777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              669 RV-----GNDKI-ASAKIEGKTLKVTGKTAGVTDVILTKDGATAGH-ATITVTQENIQIT 721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6 EELF--TGVVPIL---VELDGDVNGHKFSVSGEGEGDAT-----YGKLTLKFI 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             97
                                                                                                                                                                                                                                                                                                                                                          STRAIN-NM 105; MEDLINE-97082965; PubMed-8964497; MEDLINE-97082965; PubMed-8964497; Zhu X., MCVeigh R.R., Malathi P., Ghosh B.K.; The complete nucleotide sequence of the Bacillus licheniformis NM105 S-layer-encoding gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             49 CTTGKLPVPWPTLV-----TTLSYGVQCFSRYPDHMKQHDFFKSAMPEGYVQER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gene 173:189-194 (1996).

-1- FUNCTION: THE S-LAYER IS A PARACRYSTALLINE MONO-LAYERED ASSEMBLY
OF PROTEINS WHICH COAT THE SURFACE OF BACTERIA.

-1- SUBCELLULAR LOCATION: C211 Wall.

-1- SIBLEARITY: CONTAINS 3 S-LAYER HOMOLOGY (SLH) DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            96; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6.8%; Score 87; DB 1; Length 874; 22.8%; Pred. No. 8.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              183 YQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLLGFVTA 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         96; Indels
                                                                                                                                                                                                       Bacteria, Firmicutes; Bacillales; Bacillaceae; Bacillus.
NCBI_TaxID=1402;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EFADCA4FF27D32AF CRC64;
                                                                                              01-FEB-1996 (Rel. 33, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
S-layer protein precursor (Surface layer protein).
Bacillus licheniformis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Signal; Cell wall; S-layer; Repeat.
Signal 31 30 POTENTIAL.
CHAIN 31 874 S-LAYER PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CP51_CANGA STANDARD; PRT; 533 AA P50859; Q02312; Created) 01-0CT-1996 (Rel. 34, Last sequence update)
874 AA
                                                                  01-FEB-1996 (Rel. 33, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           92734 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; U38842; AAC44405.1; -. InterPro; IPR001119; SLH. Pfam; PF00395; SLH; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 6.8%
Best Local Similarity 22.8%
Matches 65; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  444
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                109 GHEFIFNAKLADVSAEAAYSHL--------TTPVFGKGVIYDCPNHRLM 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     80 KQHDFFKSAM-PEGYV-----QERTIFFKDDGNYKTRAEVKFEGDTLVNRIELKGIDF 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              132 KEDGNILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIRHNIEDGSVQLADHYQQNTPIGD 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25 GHKFSVS---GEGEGDATYGKLTLKFICTTGKLPVPWPTLVTTLSYGVQCFSRYDDH--M 79
                                                                                                                                                                                  STRAIN-2001-L5;
MEDLINE-96161286; PubMed-8593007;
Geber A., Hitchcock C.A., Swartz J.E., Pullen F.S., Marsden K.E.,
Kwon-Chung K.J., Bennett J.E.;
Poeletion of the Candida glabrata ERG3 and ERG11 genes: effect on cell
viability, cell growth, sterol composition, and antifungal
susceptibility.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         : | | | : | : | : | : | : | | 150 EQKKFVKGALTKEAFVRYYYPLIAEEIYKYFRNSKNFKINENNSGIVDVMVSQPEM--TIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    208 TASRSILGKEMEDKIDFAYLYSDLDKGFTPINF-VFPNLPLEHYRKEDHAQQAIS---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Torulopsis (Candida) glabrata in clinical specimens by specials-special constead PCR amplification of a cytochrome P-450 lanosterol-alpha-demethylase (LiA1) gene fragment.";
J. Clin. Microbiol. 32:1902-1907(1994).
-!- FUNCTION: CAPALYSES C14-DEMETHYLATION OF LANOSTEROL WHICH IS CRITICAL FOR ERGOSTEROL BIOSYNTHESIS. IT TRANSFORMS LANOSTEROL INTO 4,4'-DIMETHYL CHOLESTA-8,14,24-TRIENE-3-BETA-OL
                                                                                                                                                                                                                                                                                                                                                                                                                    <sup>ب</sup>
:
5-JUN-2002 (Rel. 41, Last annotation update)
/tochrome P450 51 (EC 1.14.14.-) (CYPL1) (P450-L1A1) (Sterol 14-lpha-demethylase) (Lanosterol 14-alpha demethylase) (P450-14DM)
                                                                                            Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        49;
                                                                                                                                                                                                                                                                                                                                                                           STRAIN-ATCC 2001;
MEDLINE-95081364; PubMed-7989540;
Burgener-Kairuz P., Zuber J.P., Jaunin P., Buchman T.G., Bille
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS00086; CYTOCHROME_P450; 1.
Electron transport; Oxidoreductase; Monooxygenase; Membrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1; Length 533;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Rapid detection and identification of Candida albicans and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        81; Indels
                                                                      Candida glabrata (Yeast) (Torulopsis glabrata).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharon
Saccharomycetales; mitosporic Saccharomycetales; Candida.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      I -> M (IN REF. 2).
I -> T (IN REF. 2).
A0506C17507E6EF7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -1- PATHWAY: Ergosterol blosynthesis.
-1- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                      Antimicrob. Agents Chemother. 39:2708-2717(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. 5.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      32; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ch 6.8%; Score 86.5; 1 Similarity 21.4%; Pred. No. 5.744; Conservative 32; Mismatche.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HEME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61305 MW;
                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 60-473 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      blosynthesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             533 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                               NCBI_TaxID=5478;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         149 HNVYIMADKQK-NGIKVNFKIRHNIEDGSVQLADHYQQ-----NTPIGDGPVLL 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             543 RNLYIQSMKFKGNGIKIN------DFDFSFGWNYNSLNRGYFPIKGVKASLG-GRVII 593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Whole-genome random sequencing and assembly of Haemophilus influenzae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  : || : || : || :| | 427 IGYGTESGISYQASVKQDNFLGTGAAVSIAGTKNDYGTSVNLGYTEPYFTKDGVSLGGNV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               487 FFENYDNSKSDISSNYKRITIGSNVIL-GFPVNENNSYYVGLGHIYNKISNFALEYN---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PEDEINE ROYA (RW20 / ATCC 51907;
MEDLINE-95350630; PubMed-7542800;
MEDLINE-95350630; PubMed-7542800;
MEDLINE-95350630; PubMed-7542800;
MELINE-95350630; PubMed-7542800;
MELINE-95350630; PubMed-7542800;
MELINE-10. White O.J. Tomb J.F., Dougherty B.A., Merrick J.M., McRenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D., Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M., Welden J.E., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D., Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C., Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M., Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  63;
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                                                                                                                                                                                                                                                                                                                                                       01-NOV-1995 (Rel. 32, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Protective surface antigen D15 precursor (80 kDa D15 antigen)
(D-15-Ag) (Outer membrane protein D15).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
Haemophilus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL.
PROTECTIVE SURFACE ANTIGEN D15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6.8%; Score 86.5; DB 1; Length 795; 11.9%; Pred. No. 8.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Science 269:496-512(1995).
-1- SUBCELLULAR LOCATION: Outer membrane.
-1- SIMILARITY: BELONGS TO THE SURFACE ANTIGEN D15 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P--DNHYLSTQSALSKDPNEKRDHWVLLGFVTAAGITLG 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Interpro; IPR000184; Bac_surfag_D15.
Pfam; PF01103; Bac_surface_Ag; 1.
Antigen; Outer membrane; Signal; Complete proteome.
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tive 30; Mismatches
192 GPVLLPDNHYLSTQSALSKDPNEKRD 217
                                                                   ------GTYMSLIKERREKND
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                                                                                                                                                                                                                                                                                                                     01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last seq
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Haemophilus influenzae
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594 PGSDNKYYKLSADVQGFYPLDRDHLWVVSAKASAGYANG 632
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         543 RNLYIQSMKFKGNGIKTN------DFDFSFGWNYNSLNRGYFPTKGVKASLG-GRVTI 593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        65 LSYGVQCFSRYPDHMKQHDF-----RTSAMPEGYVQE-----RTI 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    487 FFENYDNSKSDTSSNYKRTTYGSNVTL-GPPVNENNSYYVGLGHTYNKISNFALEYN---
                                                                                                                                                                                                                                                                                                                                                                                                  *Outer membrane protein D15 is conserved among Haemophilus influenzae species and may represent a universal protective antigen against
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 427 IGYGTESGISYQASVKQDNFLGTGAAVSIAGTKNDYGTSVNLGYTEPYFTKDGVSLGGNV
                                                                                                                                                                                                                                                                                                                                                                         Loosmore S.M., Yang Y.P., Coleman D.C., Shortreed J.M., England D.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                       STRAIN-Serotype B;
MEDLINE-95255676; PubMed-7737523;
Flack F.S., Loosmore S., Chong P., Thomas W.R.;
The sequencing of the 80-kDa D15 protective surface antigen of
Haemophilus influenzae.";
Gene 156:97-99(1995).
                                                                                       01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Protective surface antigen D15 precursor (80 kDa D15 antigen)
(D-15-Ag) (Outer membrane protein D15).
                                                                                                                                                            Haemophilus influenzae.
Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1; Length 797;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROTECTIVE SURFACE ANTIGEN D15.
2F93DE538696AF1B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Infect. Immun. 65:3701-3707(1997).
-1- SUBCELLULAR LOCATION: Outer membrane.
-1- SIMILARITY: BELONGS TO THE SURFACE ANTIGEN D15 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               78; Indels
594 PGSDNKYYKLSADVQGFYPLDRDHLWVVSAKASAGYANG 632
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21.9%; Pred. No. 8.7;
tve 30; Mismatches
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                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN-Minna, and Eagan / Serotype B;
MEDLINE-97427952; Pubmed-9284140;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR000184; Bac_surfAg_D15. Pfam; PF01103; Bac_surface_Ag; 1.
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                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                               nvasive disease.
                                                                                                                                                                                                   NCBI_TaxID-727;
                                                                                                                                                                                                                                                                                                                                                                                       Klein M.H.;
                                                                  D151_HAEIN
P46024;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -1- FUNCTION: Catalyzes the formation of 5-methyl-uridine at position 54 (M-5-U54) in all tRNA (By similarity).
-1 CATALYIC ACTIVITY: S-adenosyl-L-nionine + tRNA - S-adenosyl-L-homocysteine + tRNA containing thymine.
-1. SIMILARITY: BELONGS TO THE RNA MSU METHYLTRANSFERASE FAMILY. TRWA
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                                                                                                                                                                                                                                             Campylobacter jejuni.
Bacteria; Proteobacteria; epsilon subdivision; Campylobacter group;
                                                                     15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-Junecil-5-)-methyltransferase (EC 2.1.1.35) (tRNA(M-5-U54)-TRNA OR CJ0831C.
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CEC5328347CEE497 CRC64;
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PROSITE; PS01231; TRWA_2; FALSE_NEG
                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-NCTC 11168;
MEDLINE-20150912; Pubmed-10688204;
                                                         15-JUN-2002 (Rel. 41, Created)
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42276 MW;
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STANDARD;
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357 AA;
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the European Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               58 WPTLVTTLSYGVQCFSRYPDHMKQH-----DFFKSAMPEGYVQERT----IFFKDDGNYK 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | :: :|| :: :|| | :: :|| | :: :|| | :: :|| | :: :|| | :: :|| | :: :|| | :: :|| | :: :|| | :: :|| | :: :|| | :: :|| | :: :|| | :: :|| | :: :|| | :: :|| | :: :|| | :: :|| | :: :|| | :: :|| | :: :|| | :: :|| | :: :|| | :: :|| | :: :|| | :: :|| | :: :|| | :: :|| | :: :|| | :: :|| | :: :|| | :: :|| | :: :|| | :: :|| | :: :|| | :: :|| | :: :|| | :: :|| | :: :|| | :: :|| | :: :|| | :: :|| | :: :|| | :: :|| | :: :|| | :: :|| | :: :|| | :: :|| | :: :|| | :: :|| | :: :|| | :: :|| | :: :|| | :: :|| | :: :|| | :: :|| | :: :|| | :: :|| | :: :|| | :: :|| | :: :|| | :: :|| | :: :|| | :: :|| | :: :|| | :: :|| | :: :|| | :: :|| | :: :|| | :: :|| | :: :|| | :: :|| | :: :|| | :: :|| | :: :|| | :: :|| | :: :|| | :: :|| | :: :|| | :: :|| | :: :|| | :: :|| | :: :|| | :: :|| | :: :|| | :: :|| | :: :|| | :: :|| | :: :|| | :: :|| | :: :|| | :: :|| | :: :|| | :: :|| | :: :|| | :: :|| | :: :|| | :: :|| | :: :|| | :: :|| | :: :|| | :: :|| | :: :|| | :: :|| | :: :|| | :: :|| | :: :|| | :: :|| | :: :|| | :: :|| | :: :|| | :: :|| | :: :|| | :: :|| | :: :|| | :: :|| | :: :|| | :: :|| | :: :|| | :: :|| | :: :|| | :: :|| | :: :|| | :: :|| | :: :|| | :: :|| | :: :|| | :: :|| | :: :|| | :: :|| | :: :|| | :: :|| | :: :|| | :: :|| | :: :|| | :: :|| | :: :|| | :: :|| | :: :|| | :: :|| | :: :|| | :: :|| | :: :|| | :: :|| | :: :|| | :: :|| | :: :|| | :: :|| | :: :|| | :: :|| | :: :|| | :: :|| | :: :|| | :: :|| | :: :|| | :: :|| | :: :|| | :: :|| | :: :|| | :: :|| | :: :|| | :: :|| | :: :|| | :: :|| | :: :|| | :: :|| | :: :|| | :: :|| | :: :|| | :: :|| | :: :|| | :: :|| | :: :|| | :: :|| | :: :|| | :: :|| | :: :|| | :: :|| | :: :|| | :: :|| | :: :|| | :: :|| | :: :|| | :: :|| | :: :|| | :: :|| | :: :|| | :: :|| | :: :|| | :: :|| | :: :|| | :: :|| | :: :|| | :: :|| | :: :|| | :: :|| | :: :|| | :: :|| | :: :|| | :: :|| | :: :|| | :: :|| | :: :|| | :: :|| | :: :|| | :: :|| | :: :|| | :: :|| | :: :|| | :: :|| | :: :|| | :: :|| | :: :|| | :: :|| | :: :|| | :: :|| | :: :|| | :: :|| | :: :|| | :: :|| | :: :|| | :: :|| | :: :|| | :: :|| | :: :|| | :: :|| | :: 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        109 T-------RAEVKFEGDILVNRIELKGIDFKEDGNILGHKLEYNYNSHNVYIM 154
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hydrolase; Nuclease; Endonuclease; DNA replication; DNA-binding.
SEQUENCE 788 AA; 90070 MW; FB44F38F75EADF44 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -1 - CATALYTIC ACTIVITY: N deoxynucleoside triphosphate - N diphosphate
                                                                                 01-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
P protein [Includes: DNA-directed DNA polymerase (EC 2.7.7.7); RNA-directed DNA polymerase (EC 2.7.7.49); Ribonuclease H (EC 3.1.26.4)].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-88333160; PubMed-3418788;
Sprengel R., Kaleta E.F., Will H.;
*Isolation and characterization of a hepatitis B virus endemic in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    65;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PIR; A30082; JDVLHH.
InterPro; IPR001462; DNAPOl_viral_C.
InterPro; IPR000401; DNAPOl_viral_N.
InterPro; IPR00047; KVTse.
Pfam; PF00078; rvt; 1.
Pfam; PF00078; rvt; 1.
Pfam; PF000342; DNA_POl_viral_N; 1.
ProDom; PD000814; DNAPOl_viral_C; 1.
Transferase; RNA-directed DNA POlymerase; DNA-directed DNA |
                                                                                                                                                                                                                                           Heron hepatitis b virus.
Viruses; Retroid viruses; Hepadnaviridae; Avihepadnavirus.
NCBI_TaxID=28300;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 66; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            + [DNA](N).
-!- CATALYTIC ACTIVITY: Endonucleolytic cleavage to 5'-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (Rel. 40, Created)
(Rel. 40, Last sequence update)
(Rel. 40, Last annotation update)
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19.7%; Pred. No. 10;
tive 32; Mismatches
                             788 AA.
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                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              J. Virol. 62:3832-3839(1988).
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                          STANDARD;
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16-OCT-2001 (
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032629;
                             DPOL_HPBHE
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D153_HAEIN
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                                                                                                                                                                                                                                                                                                                                                                                     "Outer membrane protein D15 is conserved among Haemophilus influenzae species and may represent a universal protective antigen against
                                                                                                                                                                                                                                                                 STRAIN-PAK 12085;
MEDLINE-97427952; PubMed-9284140;
Loosmore S.M., Yang Y.P., Coleman D.C., Shortreed J.M., England D.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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16-OCT-2001 (Rel. 40, Last annotation update)
Inter-alpha-trypsin inhibitor heavy chain H3 precursor (ITI heavy
chain H3) (HC3).
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             63;
Protective surface antigen D15 precursor (80 kDa D15 antigen) (D-15-Ag) (Outer membrane protein D15). Haemophilus influenzae. Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae; Haemophilus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL.
PROTECTIVE SURFACE ANTIGEN D15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1; Length 793;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Invasive disease.";
Infect. Immun. 65:3701-3707(1997).
-1- SUBCELLULAR LOCATION: Outer membrane.
-1- SIMILARITY: BELONGS TO THE SURFACE ANTIGEN D15 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          79; Indels
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InterPro; IPR000184; Bac_surfag_D15.
Pfam; PF01103; Bac_surface_Ag; I.
Antigen; Outer_membrane; Signal.
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15-JUL-1998 (Rel. 36, Last sequ
16-OCT-2001 (Rel. 40, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE 793 AA; 87511 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INTER-ALPHA-TRYPSIN INHIBITOR HEAVY CHAIN
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                                                                                                  heavy-chain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                           Yamamoto T., Yamamoto K., Sinohara H.;
"Inter-alpha-trypaln inhibitor and its related proteins in Syrian hamster utine and plasma."
J. Blochem. 120:145-152(1996).
-!- FUNCTION: MAY ACT AS A CARRIER OF HYALURONAN IN SERUM OR AS A BINDING PROTEIN BETWEEN HYALURONAN AND OTHER MATRIX PROTEIN, INCLUDING THOSE ON CELL SURFACES IN TISSUES TO REGULATE THE LOCALIZARION, SYNTHESIS AND DEGRADATION OF HYALURONAN WHICH ARE ESSENTIAL TO CELLS UNDERGOING BIOLOGICAL PROCESSES (BY SIMILARITY).
                                                          Nakatani T., Suzuki Y., Yamamoto T., Sinohara H.;
"Molecular cloning and sequencing of cDNAs encoding three heavy-chaip precursors of the inter-alpha-trypsin inhibitor in Syrian hamster:
implications for the evolution of the inter-alpha-trypsin inhibitor heavy chain family.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-LINKED (GLCNAC. .) (POTENTIAL).
CHONDROITIN 4-SULFATE, CROSS-LINK SITE
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N-LINKED (GLCNAC. ..) (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Serine protease inhibitor; Repeat; Signal; Multigene family;
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                                                                                                                                                                                                                                                                                   SEQUENCE OF 31-50; 446-472 AND 504-523, AND SUBUNITS
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34; Mismatches
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                                MEDLINE-97420688; PubMed-9276673;
                                                                                                                                                                                                                                                                                                                                                 MEDLINE-97018241; PubMed-8864857;
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Pfam; PF00092; vwa; 1.
SMART; SM00327; VWA; 1.
PROSITE; PS50234; VWFA; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linkages in cellulose.
-1- SIMILARITY: BELONGS TO CELLULASE FAMILY A (FAMILX 5 OF GLYCOSYL
                                                                                                                                                                                                                                                                                         97;
                                                  01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Endoglucanase precursor (EC 3.2.1.4) (Endo-1,4-beta-glucanase)
(Alkaline cellulase).
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SIMILARITY: CONTAINS 3 S-LAYER HOMOLOGY (SLH) DOMAINS.
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                                                                                                                                                                                       Bacillus sp. (strain KSM-635).
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus
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  941 AA
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33; Mismatches
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Pfam: PF00395; SLH: 3.
PROSITE: PS00659; GLYCOSYL, 1PPROL_F5; 1.
PROSITE; PS01072; SLH_DOMAIN; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; M2/420, 220043, PIR; S29043; S29043, HSSP, 085465; 3A3H. InterPro; IPR005086; CBM_17_28. InterPro; IPR001547; GH_5. TPR00119; SLH.
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49; Conserv
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Query Match
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                     --EKRDHMVLL 222
                                                             ----PKNHYIIWELANEPSPNNNGGPGLINDERGWEAVKEYAEPIVEMLREKGDNMILV 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-91273991; PubMed-2054189;
MEDLINE-91273991; PubMed-2054189;
Wendland B., Miller K.G., Schilling J., Scheller R.H.;
Wendland B., Miller K.G., Schilling J., Scheller R.H.;
"Differential expression of the p65 gene family.";
Neuron 6:993-1007(1991).
-!- FUNCTION: MAY HAVE A REGULATORY ROLE IN THE MEMBRANE INTERACTIONS DURING TRAFFICKING OF SYNAPTIC VESICLES AT THE ACTIVE ZONE OF THE SYNAPSE. IT BINDS ACIDIC PHOSPHOLIPIDS WITH A SPECIFICITY THAT REQUIRES THE PRESENCE OF BOTH AN ACIDIC HEAD GROUP AND A DIACYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -1- SUBUNIT: HOMODIMER OR HOMOTRIMER (POSSIBLE).
-1- SUBCELLULAR LOCATION: SYNAPTIC VESICLES IN NEURONS.
-1- TISSUE SPECIFICITY: SPINAL CORD, BRAINSTEM, MIDBRAIN AND ELECTRIC
                                                                                                                                                                                                                                                                                                                                                                                                                                Discopyge ommata (Electric ray).
Eukaryota, Metazoa, Chordata, Craniata; Vertebrata; Chondrichthyes;
Elasmobranchii; Squalea; Hypnosqualea; Pristiorajea; Batoidea;
Torpediniformes; Narchooldel; Narcholdee; Discopyge.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C2 DOMAIN 1.
C2 DOMAIN 2.
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
2033F05FD8C69F39 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SMART; SM00239; C2; 2.
PROSITE; PS00499; C2_DOMAIN_1; 2.
PROSITE; PS00499; C2_DOMAIN_2; 2.
Transmembrane; Repeat; Synapse; Multigene family; Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CYTOPLASMIC (POTENTIAL). PHOSPHOLIPID BINDING (PROBABLE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -i- SIMILARITY: CONTAINS 2 C2 DOMAINS.
-i- SIMILARITY: BELONGS TO THE SYNAPTOTAGMIN FAMILY.
                                                                                                                                                                                                                                                                                                                                        01-MAR-1992 (Rel. 21, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
Synaptotagmin B (Synaptic vesicle protein O-P65-B).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VESICULAR (POTENTIAL).
POTENTIAL.
                                                                                                                                                                                                                                                                       439 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HSSP; P21707; IBYN.
InterPro; IPR000008; C2.
InterPro; IPR002149; LRI.
InterPro; IPR001565; Synaptotagmin.
Pfam; PF00168; C2; 2.
                     GPVLLPDNHYLSTQSALSKDPN-
                                                                                                                                                                                                                                                                                                                  01-MAR-1992 (Rel. 21, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRINTS; PR00360; C2DOMAIN.
PRINTS; PR00399; SYNAPTOTAGMN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     49278 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; M64276; AAA49228.1; -. PIR; JH0414; JH0414.
                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    101
439
399
395
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID-7785;
                                                                                                          223 G 223
                                                                                                                                                        416 G 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BACKBONE.
                                                                                                                                                                                                                                                                                                                                     01-MAR-1992
01-NOV-1995
                                                                                                                                                                                                                                                                       SY62_DISOM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGAN
                                                             361
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TRANSMEM
                   192
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
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SY62_DISOM
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                                                                                           12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               150 -NVYIMADKQKN-GIKVN------FKIRHNIEDGSVQLA----DHYQQNTFI 189
                                                                                                                                                                                      69
                                                                                                                                                                                                                                                                        96
                                                                                                                                                                                                                                      38 MMPIDTGDNSTEAGVPGEGKND-VFEKLKEKFMNELQKIPLPPWALIAIAIVSGLLLLTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          --DILVNRIELKGIDFKEDGNI--LGHKLEYNYNSH-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16 LVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPV-PWPTLVTTLSYGV----
                                                                                                                                                                                                                                                                                                                                                                    70 -----QCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                          97 CLCICKKCCCKKKKKKKEKGKGK-------KNDINMK---DVKGSGGNQDDD
                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "The complete genome sequence of the murine respiratory pathogen Mycoplasma pulmonis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; 1rnv. | Interpro; Interpro; 1rnv. | Interpro; Interpro
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Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
NCBI_TaxID=2107;
                                                                                           92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chambaud I., Heilig R., Ferris S., Barbe V., Samson D., Galis
Moszer I., Dybvig K., Wroblewski H., Viari A., Rocha E.P.C.,
Blanchard A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 84.5; DB 1; Length 613; Pred. No. 9.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               190 GDGPVLLPD-----NHYLSTQSALSKDPNEKRDHMVLLGFVTAAG 229
    DB 1; Length 439;
                                                                                           94; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUCLEIC ACIDS RES. 29:2145-2153(2001).
-!- COFACTOR: BINDS 1 ZINC ION (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Oligoendopeptidase F homolog (EC 3.4.24.-).
PREPF OR MYPU_3210.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ş
                                                                                      46; Mismatches
6.7%; Score 85;
19.2%; Pred. No. 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MypuList; MYPU_3210; ...
InterPro; IPR001567; Peptidase_M3.
InterPro; IPR000130; Zn_MTpeptdse.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AL445564; CAC13494.1; -.
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                                      Similarity 19.2
5; Conservative
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Best Local Similarity
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                                                                                           55;
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                                                Best Local
Matches
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.,	124	99	176	115	231	164			
Gaps	TLVNRI	SKYONI	NIEDGS	OIGDEN	TAAGIT	:: KVS			
29;	KFEGD	KIK-D		YSFFN	LLGFV				
Indels	SNYKTRAEV	:: : FLEKSKKLI	IKVNFKIRH	I SQKFEFMY	PNEKRDHMV	EVEDYLI			
75;	FFKDD		KOKNG	SHFRE	SALSKD	IRLSK-			
Mismatches	SAMPEGYVQERTI	: DYLLEGKTIDQLE	NY NSHINVY I - MAL	NY ISNNISVNVVI	DNHYLSTOS	KKALDFVFKSKKHRLSKEVEDYLI			90:06
40;	HDFFK	: I	HKLEY	: I : NKI-I	VLLP-	RLASY			, 15:
44; Conservative 40; Mismatches 75; Indels 29; Gaps	65 LSYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLVNRI 124	HERTRIA STATE HERT HERTRIA STATE HERTR	125 ELKGIDFKEDGNILGHKLEYNYNSHNVYI-MADKQKNGIKVNFKIRHNIEDGS 176	57 ESYLESLKLEEDFULLNNKI-INYISNNISVNVVDSHFREISQKFEFMYSFFNQIGDEN 115	177 VQLADHYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLLGFVTAAGIT 231	:: : :: ::	232 LGMDELYK 239	165 RGNIELYK 172	Search completed: June 3, 2003, 15:07:06 Job time: 24 secs
44;	65 1.5	X.	.25 E-	57 ES	77 VC	16 01	32 16	65 RG	leted 24 se
Matches	Qy	Op	0у	qa	0у 1	Db 1	0у 2	Db 1	Search completed: Job time : 24 secs